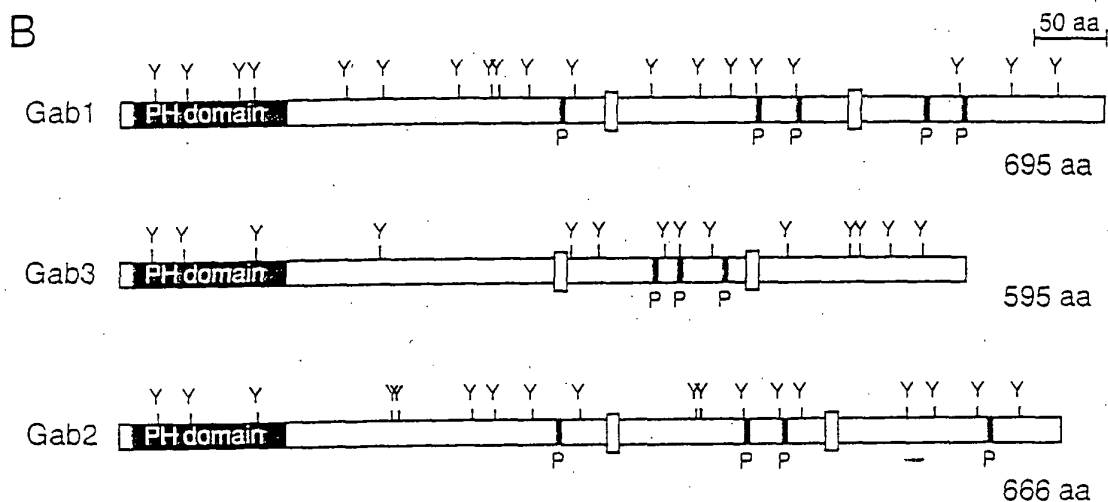


A

Human	MSAGDAVCTGWLVKSPPERKLQRYAWKRWEVLRRGRMSGNPDVLEYRKNKHSKPIRVI	60
Murine	MSTGDTVCMGWLIKSPPERKLQRYAWKRWEVLRRGRMSGNPDVLEYRKNKHSNKPIRVI	60
	**:*:*:* ***:*****	
Human	DLSECAVWKHVGPSFVRKEFQNNFVIVKTTSRFTFYLVAKTEQEMQVWVHSISQVCNGLGH	120
Murine	DLSECTVWKHAGPGFIRKEFQKNFVIVKTTSRFTFYLVAKTEEMQVWVHSISQVCNESH	120
	*****:*****.*:*:*:*:*:*****:*****:*****:*****:*****	
Human	LEDGADSMESLSYTPSSLPSSASSLLTAHAASSSLPRDDPNTNAVATEETRSESELLFL	180
Murine	LEDGADSMESLSHMPSSFQPSFASSLHTFVHVANSALLKDDGNTNSVVTETTRSEFLFL	180
	*****:*****:***:*	
Human	PDYLVLSNCETGRLHHTSLPTRCDSWSNSDRSLEQASFDVDFVDCLOPLPSSHLVHPSCH	240
Murine	PDYLILSNCETGRLHHASLPTRCDSWSNSNHSLAQTSFDDVFLDGLQPFISNNLVHPLHH	240
	****:*****:*****:*****:*****:*****:*****:*****:*****	
Human	GSGAQEVPSRRPQAALIWSREINGPPRDHLSSSPLESSLSSTIQVDKNQGSPLPCGAKEL	300
Murine	GKVSQDFPSIRPQASLIWNREINGPSRNLMS SSPLESSLNPTVHVEEKQVSLPSGVKEL	300
	*:*	
Human	DIMSNTPPPRPPKPSHLSERRQEE--WSTHSGSKKPECTLVPRRISLSGLDNMRTWKADV	358
Murine	NIMSNTPPPRPPKPSYLSEQRQDQPLLTHGSSNKKPGYTMVPRRISLSGLDHVGSWKGDV	360
	:*****:*****:*****:*****:*****:*****:*****:*****:*****	
Human	EGQSLRHRDKRLSLNLPCKRFS <sup>p85?</sup> PMYPTASASIEDSYV <sup>p85?</sup> PMSE <sup>p85?</sup> QAGASGLGPHCSPDDYIPMN	418
Murine	QSQSLRHRDKRLSLNLPCKRFS <sup>p85?</sup> PIYPTASPSAEDSYV <sup>p85?</sup> PMSE <sup>p85?</sup> KGTASELRPHCSQDDYIPMS	420
	:*****:*****:*****:*****:*****:*****:*****:*****:*****	
Human	SGSISSPLPELPANLEPPPVNRLDKPQKRSRPPPLDLRNLSTIREHASLTRTRTVPCSR	478
Murine	S----SMLPELPADLEPPPVNRLDKPQKRSRPPPLDSRNLSTIQEHTSLTRTYTVPCNRT	476
	* * *****:*****:*****:*****:*****:*****:*****:*****	
Human	SFLSPERNGINARSFFANPVSREDEES <sup>p85?</sup> -----YIEMEERTASSLSGALTWTK	527
Murine	SFLSPQRNGINCARLFSTPSEEEEEEEEEEEEEEEEEKYIQMEYGTVSSLSRSALSWTK	536
	*****:*****.*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*	
Human	<sup>SHP2</sup> KFSLDYALDFNSASPAPMQKLLLSEEQRVDYVQVDEQKTQALQSTKQEWTDERQSKV	586
Murine	<sup>SHP2</sup> KFSLDYALDFNSTSPAPVQKLLLSEEQRVDYVQVDEQKTQAFRSTKQAWTDERQSKV	595
	*****:*****:*****:*****:*****:*****:*****:*****:*****	

Figure 1A



**C**

Gab3	MSTG--D-TVCMGWLKSPPERKLQRYAWRKRWFVLRGR	37
Gab2	MSGGGGDDVCTGWLKSPPEKKLRRYAWKKRWFILRSGR	40
Gab1	MSGG--E-VVCSGWLKSPPEKKLKRYAWKRRWFVLRSGR	37
	** * : . ** *** *****:***:*****::*****: ** **	
Gab3	MSGNPDVLEYYRNKHSNKPIRVIDLSECTVWKHAGPGFIR	77
Gab2	MSGDPDVLEYYKNEHSKKPLRIINLNLCEQVD-AGLTFNK	79
Gab1	LTGDPDVLEYYKNDHAKKPIRIIDLNLCCQVD-AGLTFNK	76
	::*:*****:*.*::*:*:*:*:*. * . ** *	
Gab3	KEFQKNFVFIVKTTSRTFYLVAKTEEEMQVWVHSISQVCN	117
Gab2	KELQDSFVFDIKTSERTFYLVAETEAMNKWVQSICQICG	119
Gab1	KEFENSYIFDINTIDRIFYLVADSEEDMNKWWRCICDICG	116
	**::*:*:*. * *****:*:*: **::*::*.	

Figure 1B and C